

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/511,719A
Source: TFW16
Date Processed by STIC: 02/27/2007

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/511, 719A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,719A

DATE: 02/27/2007
TIME: 11:08:37

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

2 <110> APPLICANT: REGEN Biotech. Inc.
4 <120> TITLE OF INVENTION: The method for measuring the amount of Beta1 protein and diagnostic kit
5 using the same
7 <130> FILE REFERENCE: 2fpo-10-14
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/511,719A
C--> 9 <141> CURRENT FILING DATE: 2004-11-26
9 <160> NUMBER OF SEQ ID NOS: 12
11 <170> SOFTWARE: KopatentIn 1.71

Does Not Comply
Corrected Diskette Needed

CP9-1-11

ERRORED SEQUENCES

13 <210> SEQ ID NO: 1
14 <211> LENGTH: 683
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
19 Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu
E--> 20 1 5 10 15
22 Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
E--> 23 20 25 30
25 Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
E--> 26 35 40 45
28 Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
E--> 29 50 55 60
31 Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
E--> 32 65 70 75 80
34 Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
E--> 35 85 90 95
37 Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
E--> 38 100 105 110
40 Val Gly Ser Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
E--> 41 115 120 125
43 Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
E--> 44 130 135 140
46 Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val. Leu Asp Ser Leu Val
E--> 47 145 150 155
49 Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
E--> 50 165 170 175
52 Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
E--> 53 180 185 190
55 Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
E--> 56 195 200 205

Invalid
Amino
Acid
Number
See glossary
on Error
Summary
Sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,719A

DATE: 02/27/2007
TIME: 11:08:37

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

58 Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
E--> 59 210 215 220
61 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
E--> 62 225 230 235 240
64 Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
E--> 65 245 250 255
67 Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
E--> 68 260 265 270
70 Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
E--> 71 275 280 285
73 Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
E--> 74 290 295 300
76 Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
E--> 77 305 310 315 320
79 Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
E--> 80 325 330 335
82 Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
E--> 83 340 345 350
85 Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
E--> 86 355 360 365
88 Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
E--> 89 370 375 380
91 Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
E--> 92 385 390 395 400
94 Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
E--> 95 405 410 415
97 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
E--> 98 420 425 430
100 Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
E--> 101 435 440 445
103 Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
E--> 104 450 455 460
106 Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
E--> 107 465 470 475 480
109 Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
E--> 110 485 490 495
112 Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
E--> 113 500 505 510
115 Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
E--> 116 515 520 525
118 Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
E--> 119 530 535 540
121 Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
E--> 122 545 550 555 560
124 Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
E--> 125 565 570 575
127 Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
E--> 128 580 585 590
130 Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val

*Dame
Wend*

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

E--> 131 595 600 605
133 Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
E--> 134 610 615 620
136 Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
E--> 137 625 630 635 640
139 Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
E--> 140 645 650 655
142 Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
E--> 143 660 665 670
145 Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
E--> 146 675 680
246 <210> SEQ ID NO: 3
247 <211> LENGTH: 585
248 <212> TYPE: PRT
249 <213> ORGANISM: Homo sapiens
251 <220> FEATURE:
252 <221> NAME/KEY: PEPTIDE
253 <222> LOCATION: (1)..(585)
254 <223> OTHER INFORMATION: 69 to 653 amino acid sequence of human ID No.1
257 <400> SEQUENCE: 3
258 Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys
E--> 259 1 5 10 15
261 Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala
E--> 262 20 25 30
264 Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr
E--> 265 35 40 45
267 Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met
E--> 268 50 55 60
270 Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp
E--> 271 65 70 75 80
273 Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn
E--> 274 85 90 95
276 Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val
E--> 277 100 105 110
279 Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln
E--> 280 115 120 125
282 Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val
E--> 283 130 135 140
285 Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val
E--> 286 145 150 155 160
288 Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln
E--> 289 165 170 175
291 Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val
E--> 292 180 185 190
294 Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr
E--> 295 195 200 205
297 Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr
E--> 298 210 215 220
300 Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn

Same
Entry

RAW SEQUENCE LISTING
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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

E--> 301	225	230	235	240
303	Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly			
E--> 304		245	250	255
306	Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser			
E--> 307		260	265	270
309	Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp			
E--> 310		275	280	285
312	Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile			
E--> 313		290	295	300
315	Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val			
E--> 316	305	310	315	320
318	Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu			
E--> 319		325	330	335
321	Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe			
E--> 322		340	345	350
324	Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg			
E--> 325		355	360	365
327	Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly			
E--> 328		370	375	380
330	Gln Thr Leu Glu Thr Leu Gly Lys Lys Leu Arg Val Phe Val Tyr			
E--> 331	385	390	395	400
333	Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys			
E--> 334		405	410	415
336	Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro			
E--> 337		420	425	430
339	Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser			
E--> 340		435	440	445
342	Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn			
E--> 343		450	455	460
345	Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg			
E--> 346	465	470	475	480
348	Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu			
E--> 349		485	490	495
351	Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser			
E--> 352		500	505	510
354	Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys			
E--> 355		515	520	525
357	Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro			
E--> 358		530	535	540
360	Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile			
E--> 361	545	550	555	560
363	Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp			
E--> 364		565	570	575
366	Glu Leu Ala Asp Ser Ala Leu Glu Ile			
E--> 367		580	585	
439	<210> SEQ ID NO: 5			
440	<211> LENGTH: 609			
441	<212> TYPE: PRT			
442	<213> ORGANISM: Mouse Intracisternal A-particle			

? see Glen's 10
on Encr Summary
Sheet.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,719A

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

444 <220> FEATURE:
445 <221> NAME/KEY: PEPTIDE
446 <222> LOCATION: (1)..(609)
447 <223> OTHER INFORMATION: 23 to 641 amino acid sequence of mouse
450 <400> SEQUENCE: 5
451 Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu Val Leu Gln His Ser Arg
E--> 452 1 5 10 15
454 Leu Arg Gly Arg Gln His Gly Pro Asn Val Cys Ala Val Gln Lys Val
E--> 455 20 25 30
457 Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn Cys Lys Gln Trp Tyr Gln
E--> 458 35 40 45
460 Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys Cys Pro
E--> 461 50 55 60
463 Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala Leu Pro
E--> 464 65 70 75 80
466 Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr Thr Thr
E--> 467 85 90 95
470 Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met Glu Gly
E--> 471 100 105 110
473 Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp Ala Ser
E--> 474 115 120 125
476 Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn Ile Glu
E--> 477 130 135 140
479 Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val Leu Thr
E--> 480 145 150 155 160
482 Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln Asn Ser
E--> 483 165 170 175
485 Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val Asn Cys
E--> 486 180 185 190
488 Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val Val His
E--> 489 195 200 205
491 Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln Gln Ile
E--> 492 210 215 220
494 Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val Ala Ala
E--> 495 225 230 235 240
497 Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr Leu Leu
E--> 498 245 250 255
500 Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr Leu Asn
E--> 501 260 265 270
503 Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn Asn His
E--> 504 275 280 285
506 Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly Leu Ser
E--> 507 290 295 300
509 Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser Gly Asp
E--> 510 305 310 315 320
512 Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp Ile Leu
E--> 513 325 330 335
515 Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile Pro Asp
E--> 516 340 345 350

Same
End

RAW SEQUENCE LISTING
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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

518 Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val Ser Thr
E--> 519 355 360 365
521 Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu Ser Gly
E--> 522 370 375 380
524 Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe Lys Asp
E--> 525 385 390 395 400
527 Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg Asn His
E--> 528 405 410 415
530 Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly Gln Thr
E--> 531 420 425 430
533 Leu Glu Thr Leu Gly Gly Lys Leu Arg Val Phe Val Tyr Arg Asn
E--> 534 435 440 445
536 Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys Arg Gly
E--> 537 450 455 460
539 Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro Pro Met
E--> 540 465 470 475 480
542 Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu
E--> 543 485 490 495
545 Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu
E--> 546 500 505 510
548 Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu
E--> 549 515 520 525
551 Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala
E--> 552 530 535 540
554 Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly
E--> 555 545 550 555 560
557 Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu
E--> 558 565 570 575
560 Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala
E--> 561 580 585 590
563 Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn
E--> 564 595 600 605
566 Val
595 <210> SEQ ID NO: 7
596 <211> LENGTH: 140
597 <212> TYPE: PRT
598 <213> ORGANISM: Artificial Sequence
600 <220> FEATURE:
601 <223> OTHER INFORMATION: Betaig-h3 D-IV(1X) amino acid sequence
604 <400> SEQUENCE: 7
605 Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
E--> 606 1 5 10 15
608 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
E--> 609 20 25 30
611 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
E--> 612 35 40 45
614 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
E--> 615 50 55 60
617 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile

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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

E--> 618 65 70 75 80
 620 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 E--> 621 85 90 95
 623 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 E--> 624 100 105 110
 626 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 E--> 627 115 120 125
 629 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
 E--> 630 130 135 140
 633 <210> SEQ ID NO: 8
 634 <211> LENGTH: 280
 635 <212> TYPE: PRT
 636 <213> ORGANISM: Artificial Sequence
 638 <220> FEATURE:
 639 <223> OTHER INFORMATION: Betaig-h3 D-IV(2X) amino acid sequence
 642 <400> SEQUENCE: 8
 643 Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
 E--> 644 1 5 10 15
 646 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 E--> 647 20 25 30
 649 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 E--> 650 35 40 45
 652 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 E--> 653 50 55 60
 655 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 E--> 656 65 70 75 80
 658 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 E--> 659 85 90 95
 661 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 E--> 662 100 105 110
 664 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 E--> 665 115 120 125
 667 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
 E--> 668 130 135 140
 670 Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
 E--> 671 145 150 155 160
 673 Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
 E--> 674 165 170 175
 676 Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
 E--> 677 180 185 190
 679 Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
 E--> 680 195 200 205
 682 Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
 E--> 683 210 215 220
 685 Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
 E--> 686 225 230 235 240
 688 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 E--> 689 245 250 255
 691 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr

Same
End

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E--> 692 260 265 270
694 Asn Val Leu Gln Pro Pro Ala Asn
E--> 695 275 280
698 <210> SEQ ID NO: 9
699 <211> LENGTH: 420
700 <212> TYPE: PRT
701 <213> ORGANISM: Artificial Sequence
703 <220> FEATURE:
704 <223> OTHER INFORMATION: Betaig-h3 D-IV(3X) amino acid sequence
707 <400> SEQUENCE: 9
708 Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
E--> 709 1 5 10 15
711 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
E--> 712 20 25 30
714 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
E--> 715 35 40 45
717 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
E--> 718 50 55 60
720 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
E--> 721 65 70 75 80
723 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
E--> 724 85 90 95
726 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
E--> 727 100 105 110
729 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
E--> 730 115 120 125
732 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
E--> 733 130 135 140
735 Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
E--> 736 145 150 155 160
738 Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
E--> 739 165 170 175
741 Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
E--> 742 180 185 190
744 Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
E--> 745 195 200 205
747 Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly
E--> 748 210 215 220
750 Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
E--> 751 225 230 235 240
753 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
E--> 754 245 250 255
756 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
E--> 757 260 265 270
759 Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val
E--> 760 275 280 285
762 Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala
E--> 763 290 295 300
765 Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr

*Same
End*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,719A

DATE: 02/27/2007
TIME: 11:08:37

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

E--> 766 305 310 315 320
 768 Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg
 E--> 769 325 330 335
 771 Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu
 E--> 772 340 345 350
 774 Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala
 E--> 775 355 360 365
 777 Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu
 E--> 778 370 375 380
 780 Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp
 E--> 781 385 390 395 400
 783 Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln
 E--> 784 405 410 415
 786 Pro Pro Ala Asn
 787 420
 790 <210> SEQ ID NO: 10
 791 <211> LENGTH: 560
 792 <212> TYPE: PRT
 793 <213> ORGANISM: Artificial Sequence
 795 <220> FEATURE:
 796 <223> OTHER INFORMATION: Betaig-h3 D-IV(4X) amino acid sequence
 799 <400> SEQUENCE: 10
 800 Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
 E--> 801 1 5 10 15
 803 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 E--> 804 20 25 30
 806 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 E--> 807 35 40 45
 809 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 E--> 810 50 55 60
 812 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 E--> 813 65 70 75 80
 815 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 E--> 816 85 90 95
 818 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 E--> 819 100 105 110
 821 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 E--> 822 115 120 125
 824 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
 E--> 825 130 135 140
 827 Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met
 E--> 828 145 150 155 160
 830 Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg
 E--> 831 165 170 175
 833 Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala
 E--> 834 180 185 190
 836 Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu
 E--> 837 195 200 205
 839 Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly

same
gene

RAW SEQUENCE LISTING
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Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

E--> 840 210 215 220
 842 Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu
 E--> 843 225 230 235 240
 845 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 E--> 846 245 250 255
 848 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
 E--> 849 260 265 270
 851 Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val
 E--> 852 275 280 285
 854 Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala
 E--> 855 290 295 300
 857 Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr
 E--> 858 305 310 315 320
 860 Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg
 E--> 861 325 330 335
 863 Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu
 E--> 864 340 345 350
 866 Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala
 E--> 867 355 360 365
 869 Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu
 E--> 870 370 375 380
 872 Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp
 E--> 873 385 390 395 400
 875 Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln
 E--> 876 405 410 415
 878 Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu
 E--> 879 420 425 430
 881 Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala
 E--> 882 435 440 445
 884 Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala
 E--> 885 450 455 460
 887 Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg
 E--> 888 465 470 475 480
 890 Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile
 E--> 891 485 490 495
 893 Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu
 E--> 894 500 505 510
 896 Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val
 E--> 897 515 520 525
 899 Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr
 E--> 900 530 535 540
 902 Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
 E--> 903 545 550 555 560
 906 <210> SEQ ID NO: 11
 907 <211> LENGTH: 5
 908 <212> TYPE: PRT
 909 <213> ORGANISM: peptide
 911 <400> SEQUENCE: II
 912 Asn Lys Asp Ile Leu

2137 Responses can
 be either Artificial or
 Unknown, pls see Item
 10 on Error Summary
 sheet.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/511,719A

DATE: 02/27/2007
TIME: 11:08:37

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\02272007\J511719A.raw

E--> 913 1 5
916 <210> SEQ ID NO: 12
917 <211> LENGTH: 4
918 <212> TYPE: PRT
919 <213> ORGANISM: peptide
921 <400> SEQUENCE: 12
922 Glu Pro Asp Ile
923 1

E--> 927 19
E--> 930 1

Pls delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,719A

DATE: 02/27/2007

TIME: 11:08:38

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02272007\J511719A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=1
L:259 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:452 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:606 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
M:332 Repeated in SeqNo=7
L:644 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:709 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:801 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:913 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:927 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12